A Test Problem For Kidney Models

R. MEJIA, J. L. STEPHENSON, AND R. J. LeVEQUE
Section on Theoretical Biophysics, National Heart, Lung and Blood Institute,
  and Mathematical Research Branch,
National Institute of Arthritis, Metabolism and Digestive Diseases,
National Institutes of Health, Bethesda, Maryland 20205

There is a need in the literature for standard problems with which investigators may validate the numerical schemes that they apply to solve renal models. We consider the six-tube vasa recta model first described in [1] and used by Farahzad and Tewarson [2] and by Lory in [3] to be a good candidate for inclusion for a number of reasons.

First, this model is sufficiently complex to exhibit some of the characteristics of larger models such as discontinuous sources and small flows, while being small enough to be solved on any computer with a FORTRAN compiler.

Secondly, it provides a test of an algorithm's ability to conserve mass and water balance, which is required for accuracy (see [4]). Thirdly, a number of numerical methods have been used to solve it. All of these that express the difference equations in conservative form have obtained essentially the same solution, allowing for variation in the accuracy of each method. (Others have obtained solutions to the difference equations solved, but not to the differential equations.)

In [1] a centered-trapezoidal-difference approximation was used for the space derivatives and the resulting nonlinear equations were solved simultaneously using Newton's method. Farahzad and Tewarson in [2] used the same difference approximations and a sparse-matrix version of Newton's method for solution of the nonlinear equations. Lory [3] has used a multiple-shooting scheme to solve the problem. We have also solved it using both a partitioning scheme described in [5] for a multinephron model and DD04AD,[1] an adaptive finite-difference solver for two-point boundary problems [6,7].

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[1]DD04AD is a program obtained through the courtesy of Dr. I. Duff from the Computer Science and Systems Division, AERE Harwell, Oxfordshire, OX11 ORA, and used on the IBM 370 system at the National Institutes of Health after minor modifications.

Table 1 shows results for the model with a discontinuity at the junction of the inner and outer medulla (with the same parameter set as in [3] and with a jump at $x = 0.5$). Volume flows and salt and urea concentrations are shown for fluid leaving the descending limb of Henle (DL), the ascending vasa recta (AV), and the collecting duct (CD). Results with a resolution of 13, 39, and 79 space segments obtained with the partitioning scheme described in [5] are shown, as are extrapolated results for this model. The solution obtained by Lory in [3] and that obtained using DD04AD are also shown.

Table 2 shows results for a model with a linear transition zone between the inner and outer medulla as in [1,2,3]. In the transition zone each parameter is approximated linearly. For example,

$$h_{AL,1}(x) = h_{AL,1}(0.4) + \frac{h_{AL,1}(0.5) - h_{AL,1}(0.4)}{0.1}(x - 0.4),$$
$$0.4 < x < 0.5.$$

Although the estimated truncation error varies substantially, for most practical purposes a resolution of forty points seems adequate. Multiple shooting with a high-order integrator, as in [3], does not do much better, despite the small stepsize used. This may be due to errors accrued at the nodal points despite stringent convergence criteria for the Newton iterations. Certainly the solution obtained by Richardson extrapolation on two meshes is more than adequate.

It is also important to note that, whatever numerical scheme is used, the sources must be estimated accurately and consistently. A slight change in a source may lead to a significantly different solution, as illustrated by Lory in Table 1 of [3].

TABLE 1

	[1,5]	[1,5]	[3,8]	[5]	Extrapolated	[6]
N segments	13	39	6614	79	3082	86
Truncation error	5.92×10^{-3}	6.57×10^{-4}	$1. \times 10^{-15}$	1.6×10^{-4}	1.05×10^{-7}	$2.91 \times 10^{-}$
$v_{DL}(1)$	0.36381	0.36418	0.36424	0.36427	0.36430	0.36455
$C_{DL,1}(1)$	2.74868	2.74587	2.74542	2.74523	2.74502	2.74308
$C_{DL,2}(1)$	0.13743	0.13729	0.13727	0.13726	0.13725	0.13715
$v_{AV}(0)$	-5.67107	-5.67064	-5.67059	-5.67056	-5.67053	-5.67026
$C_{AV,1}(0)$	1.04889	1.04916	1.04918	1.04918	1.04919	1.04916
$C_{AV,2}(0)$	0.04640	0.04640	0.04640	0.04640	0.04640	0.04640
$v_{CD}(1)$	0.01274	0.01280	0.01280	0.01280	0.01280	0.01281
$C_{CD,1}(1)$	0.00014	0.00028	0.00030	0.00030	0.00031	0.00031
$C_{CD,2}(1)$	2.89460	2.88339	2.88290	2.88271	2.88249	2.88042

TABLE 2

	[1,2,5]	[1,5]	[5]	[6]	Extrapolated	[3,8]
N segments	10	40	80	89	3200	5071
Truncation error	$1.\times 10^{-2}$	6.25×10^{-4}	1.56×10^{-4}	8.90×10^{-6}	9.77×10^{-8}	$1.\times 10^{-15}$
$v_{DL}(1)$	0.41624	0.42752	0.42812	0.42830	0.42832	0.42834
$C_{DL,1}(1)$	2.40247	2.33910	2.33580	2.33481	2.33470	2.33460
$C_{DL,2}(1)$	0.12012	0.11695	0.11679	0.11674	0.11674	0.11673
$v_{AV}(0)$	-5.61708	-5.60631	-5.60575	-5.60558	-5.60556	-5.60554
$C_{AV,1}(0)$	1.04424	1.04381	1.04378	1.04377	1.04377	1.04376
$C_{AV,2}(0)$	0.04673	0.04674	0.04674	0.04674	0.04674	0.04674
$v_{CD}(1)$	0.01506	0.01574	0.01578	0.01580	0.01579	0.01580
$C_{CD,1}(1)$	0.01611	0.04402	0.04598	0.04658	0.04663	0.04670
$C_{CD,2}(1)$	2.49043	2.41345	2.40804	2.40641	2.40624	2.40608

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